

REGULATORY 21 DEC 2001

113

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE



22469

PATENT TRADEMARK OFFICE

Art Unit :  
Examiner :  
Serial No. : 09/807,721  
Filed : April 18, 2001  
Inventors : Henry Daniell  
              : Keith Wycoff  
Title : PRODUCTION OF  
              : ANTIBODIES IN  
              : TRANSGENIC PLASTIDS

Docket: 1463-PCT-US-00

Confirmation No.: 4041

Dated: December 21, 2001

**PRELIMINARY AMENDMENT**

Box PCT Application  
Commissioner for Patents  
Washington, DC 20231

Sir:

Prior to action on the merits of the case, kindly amend the above-identified application as follows:

**In the Specification** (Clean copy as amended)

**Please replace the last paragraph on pages 27 with the following:**

The plasmid containing the heavy chain sequence was cut with Sal I, and the plasmid containing the light chain sequence was cut with Sal I and Xho I. A Sal I/Xho I fragment containing the light chain sequence was then isolated and cloned into the Sal I site of the plasmid containing the heavy chain. The resulting bacterial clones were screened for a clone with the correct orientation (heavy chain followed by light chain with coding sequences in the same orientation). The heavy and light chain genes, with associated ribosome binding sites were then cut out together using Not I and Xba I, and cloned into the pLD vector.

**Remarks**

We respectfully request that the above-identified amendments be entered into the file of the case. The reference to Table 3 has been removed since there is no Table 3 in the Specification.

An early action on the merits of the case is respectfully requested.

Respectfully submitted,



T. Daniel Christenbury  
Reg. No. 31,750

TDC:gj  
(215) 563-1810

**In the Specification** (Marked-up Version)

**Please replace the last paragraph on pages 27 with the following:**

The plasmid containing the heavy chain sequence was cut with Sal I, and the plasmid containing the light chain sequence was cut with Sal I and Xho I. A Sal I/Xho I fragment containing the light chain sequence was then isolated and cloned into the Sal I site of the plasmid containing the heavy chain. The resulting bacterial clones were screened for a clone with the correct orientation (heavy chain followed by light chain with coding sequences in the same orientation). The heavy and light chain genes, with associated ribosome binding sites were then cut out together using Not I and Xba I, and cloned into the pLD vector. ~~The sequence between the Not I and Xho I sites of the heavy and light chain cassette is shown in Table 3.~~

REGD PCT/US 21 DEC 2001

#3

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Art Unit :  
Examiner :  
Serial No. : 09/807,721  
Filed : April 18, 2001  
Inventors : Henry Daniell  
              : Keith Wycoff  
Title : PRODUCTION OF  
              : ANTIBODIES IN  
              : TRANSGENIC PLASTIDS



22469

PATENT TRADEMARK OFFICE

Docket No.:1463-PCT-US-00

Confirmation No.: 4041

Dated: December 21, 2001

---

**STATEMENT ACCOMPANYING SEQUENCE LISTING**

Box PCT  
Commissioner for Patents  
Washington, DC 20231

Sir:

The undersigned hereby states that the Sequence Listing submitted concurrently herewith does not include matter which goes beyond the content of the application as filed and that the information recorded on the diskette submitted concurrently herewith is identical to the written Sequence Listing.

Respectfully submitted,

T. Daniel Christenbury  
Reg. No. 31, 750

TDC: gj  
(215) 563-1810



PCT/09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/807,721

DATE: 05/21/2002  
TIME: 15:54:10

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF3\05212002\1807721.raw

ENTERED

3 <110> APPLICANT: AUBURN UNIVERSITY  
4 UNIVERSITY OF CENTRAL FLORIDA  
6 <120> TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS  
8 <130> FILE REFERENCE: 1463-PCT-US-00  
10 <140> CURRENT APPLICATION NUMBER: 09/807,721

C--> 11 <141> CURRENT FILING DATE: 2001-12-21  
13 <150> PRIOR APPLICATION NUMBER: PCT/US01/06274

14 <151> PRIOR FILING DATE: 2001-02-28

16 <160> NUMBER OF SEQ ID NOS: 6

18 <170> SOFTWARE: PatentIn Ver. 2.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 2059

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (17..1381, 1409..2050)

29 <400> SEQUENCE: 1

30 tctagaggag ggattt atg ggg gtc cag ctt cag cag tca gga cct gac 49  
31 Met Gly Val Gln Leu Gln Gln Ser Gly Pro Asp

32 1 5 10

33 ctg gtg aaa cct ggg gcc tca gtg aag ata tcc tgc aag gct tct gga 97  
34 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly

35 15 20 25

36 tac aca ttc act gac tac aac ata cac tgg gtg aag cag agc cgt gga 145  
37 Tyr Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly

38 30 35 40

39 aag agc ctt gag tgg att gga tat att tat cct tac aat ggt aat act 193  
40 Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr

41 45 50 55

42 tac tac aac cag aag ttc aag aac aag gcc aca ttg act gta gac aat 241  
43 Tyr Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn

44 60 65 70 75

45 tcc tcc acc tca gcc tac atg gag ctc cgc agc ctg aca tct gag gac 289  
46 Ser Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp

47 80 85 90

48 60 65 70 75  
49 tct gca gtc tat tac tgt gca acc tac ttt gac tac tgg ggc caa ggc 337  
50 Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly

51 95 100 105

52 acc act ctc aca gtg agc tca gca tcc ccg acc agc ccc aag gtc ttc 385  
53 Thr Thr Leu Thr Val Ser Ser Ala Ser Pro Thr Ser Pro Lys Val Phe

54 110 115 120

55 60 65 70 75  
56 ccg ctg agc ctc gac agc acc ccc caa gat ggg aac gtg gtc gca 433

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/807,721

DATE: 05/21/2002  
TIME: 15:54:10

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF3\05212002\I807721.raw

63 Pro Leu Ser Leu Asp Ser Thr Pro Gln Asp Gly Asn Val Val Val Ala  
64 125 130 135  
66 tgc ctg gtc cag ggc ttc ttc ccc cag gag cca ctc agt gtg acc tgg 481  
67 Cys Leu Val Gln Gly Phe Phe Pro Gln Glu Pro Leu Ser Val Thr Trp  
68 140 145 150 155  
70 agc gaa agc gga cag aac gtg acc gcc aga aac ttc cca cct agc cag 529  
71 Ser Glu Ser Gly Gln Asn Val Thr Ala Arg Asn Phe Pro Pro Ser Gln  
72 160 165 170  
74 gat gcc tcc ggg gac ctg tac acc acg agc cag ctg acc ctg ccg 577  
75 Asp Ala Ser Gly Asp Leu Tyr Thr Ser Ser Gln Leu Thr Leu Pro  
76 175 180 185  
78 gcc aca cag tgc cca gac ggc aag tcc gtg aca tgc cac gtg aag cac 625  
79 Ala Thr Gln Cys Pro Asp Gly Lys Ser Val Thr Cys His Val Lys His  
80 190 195 200  
82 tac acg aat tcc agc cag gat gtg act gtg ccc tgc cga gtt ccc cca 673  
83 Tyr Thr Asn Ser Ser Gln Asp Val Thr Val Pro Cys Arg Val Pro Pro  
84 205 210 215  
86 cct ccc cca tgc tgc cac ccc cga ctg tcg ctg cac cga ccg gcc ctc 721  
87 Pro Pro Pro Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu  
88 220 225 230 235  
90 gag gac ctg ctg tta ggt tca gaa gcg aac ctc acg tgc aca ctg acc 769  
91 Glu Asp Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr  
92 240 245 250  
94 ggc ctg aga gat gcc tct ggt gcc acc ttc acc tgg acg ccc tca agt 817  
95 Gly Leu Arg Asp Ala Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser  
96 255 260 265  
98 ggg aag agc gct gtt caa gga cca cct gag cgt gac ctc tgt ggc tgc 865  
99 Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys  
100 270 275 280  
102 tac acg gtg tca tca gta ctt cct ggc tgt gcc cag cca tgg aac cat 913  
103 Tyr Ser Val Ser Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His  
104 285 290 295  
106 ggg gag acc ttc acc tgc act gct gcc cac ccc gag ttg aag acc cca 961  
107 Gly Glu Thr Phe Thr Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro  
108 300 305 310 315  
110 cta acc gcc aac atc aca aaa tcc gga aac aca ttc cgg ccc gag gtc 1009  
111 Leu Thr Ala Asn Ile Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu Val  
112 320 325 330  
114 cac ctg ctg ccg ccg tcg gag gag ctg gcc ctg aac gag ctg gtg 1057  
115 His Leu Leu Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val  
116 335 340 345  
118 acg ctg acg tgc ctg gca cgt ggc ttc agc ccc aag gat gtg ctg gtt 1105  
119 Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val  
120 350 355 360  
122 cgc tgg ctg cag ggg tca cag gag ctg ccc cgc gag aag tac ctg act 1153  
123 Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr  
124 365 370 375  
126 tgg gca tcc cgg cag gag ccc agc cag ggc acc acc acc tat gct gtg 1201  
127 Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Tyr Ala Val

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/807,721

DATE: 05/21/2002  
TIME: 15:54:10

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF3\05212002\I807721.raw

128	380	385	390	395
130	acc agc ata ctg cgc gtg gca gcc gag gac tgg aag aag ggg gag acc			1249
131	Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Glu Thr			
132	400	405	410	
134	ttc tcc tgc atg gtg ggc cac gag gcc ctg ccg ctg gcc ttc aca cag			1297
135	Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln			
136	415	420	425	
138	aag acc atc gac cgc ttg gcg ggt aaa ccc acc cat atc aat gtg tct			1345
139	Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser			
140	430	435	440	
142	gtt gtc atg gcg gag ggc acc tgc tac aga tgaaatattg			1391
143	Val Val Met Ala Glu Ala Asp Gly Thr Cys Tyr Arg			
144	445	450	455	
146	cggatccgga gggattt atg gac att gtg atg acc cag tct cca gca atc			1441
147	Met Asp Ile Val Met Thr Gln Ser Pro Ala Ile			
148	460	465		
150	atg tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc			1489
151	Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser			
152	470	475	480	
154	tca atg gta agt tac atg cac tgg ttc cag cag aag cca ggc act tct			1537
155	Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser			
156	485	490	495	
158	ccc aaa ctc tgg ctt tat agc aca tcc aac ctg gct tct gga gtc cct			1585
159	Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro			
160	500	505	510	
162	gct cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc			1633
163	Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile			
164	515	520	525	530
166	agc cga atg gag gct gaa gat gct gcc act tat tac tgc cat caa agg			1681
167	Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg			
168	535	540	545	
170	act agc tac cca tac aca ttc gga ggg ggg acc aag ctt gag atc aaa			1729
171	Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys			
172	550	555	560	
174	cga act gtg gct gca cca tct gtc atc ttc ccg cca tct gat gag			1777
175	Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu			
176	565	570	575	
178	cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc			1825
179	Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe			
180	580	585	590	
182	tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa			1873
183	Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln			
184	595	600	605	610
186	tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gag agc			1921
187	Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser			
188	615	620	625	
190	acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag			1969
191	Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu			
192	630	635	640	

RAW SEQUENCE LISTING DATE: 05/21/2002  
 PATENT APPLICATION: US/09/807,721 TIME: 15:54:10

Input Set : A:\PTO.VSK.txt  
 Output Set: N:\CRF3\05212002\I807721.raw

194 aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 2017  
 195 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 196 645 650 655  
 198 ccc gtc aca aag agc ttc aac agg gga gag tgt tgatctaga 2059  
 199 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 200 660 665  
 203 <210> SEQ ID NO: 2  
 204 <211> LENGTH: 669  
 205 <212> TYPE: PRT  
 206 <213> ORGANISM: Homo sapiens  
 208 <400> SEQUENCE: 2  
 209 Met Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly  
 210 1 5 10 15  
 212 Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp  
 213 20 25 30  
 215 Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu Glu Trp  
 216 35 40 45  
 218 Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn Gln Lys  
 219 50 55 60  
 221 Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr Ser Ala  
 222 65 70 75 80  
 224 Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr  
 225 85 90 95  
 227 Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val  
 228 100 105 110  
 230 Ser Ser Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Asp  
 231 115 120 125  
 233 Ser Thr Pro Gln Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly  
 234 130 135 140  
 236 Phe Phe Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln  
 237 145 150 155 160  
 239 Asn Val Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp  
 240 165 170 175  
 242 Leu Tyr Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro  
 243 180 185 190  
 245 Asp Gly Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Ser Ser  
 246 195 200 205  
 248 Gln Asp Val Thr Val Pro Cys Arg Val Pro Pro Pro Pro Cys Cys  
 249 210 215 220  
 251 His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu  
 252 225 230 235 240  
 254 Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala  
 255 245 250 255  
 257 Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val  
 258 260 265 270  
 260 Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser  
 261 275 280 285  
 263 Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr Phe Thr  
 264 290 295 300

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/807,721

DATE: 05/21/2002  
TIME: 15:54:10

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF3\05212002\I807721.raw

266 Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala Asn Ile  
267 305 310 315 320  
269 Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro  
270 325 330 335  
272 Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu  
273 340 345 350  
275 Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly  
276 355 360 365  
278 Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln  
279 370 375 380  
281 Glu Pro Ser Gln Gly Thr Thr Tyr Ala Val Thr Ser Ile Leu Arg  
282 385 390 395 400  
284 Val Ala Ala Glu Asp Trp Lys Lys Gly Glu Thr Phe Ser Cys Met Val  
285 405 410 415  
287 Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg  
288 420 425 430  
290 Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser Val Val Met Ala Glu  
291 435 440 445  
293 Ala Asp Gly Thr Cys Tyr Arg Met Asp Ile Val Met Thr Gln Ser Pro  
294 450 455 460  
296 Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser  
297 465 470 475 480  
299 Ala Ser Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly  
300 485 490 495  
302 Thr Ser Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly  
303 500 505 510  
305 Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu  
306 515 520 525  
308 Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His  
309 530 535 540  
311 Gln Arg Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu  
312 545 550 555 560  
314 Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
315 565 570 575  
317 Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
318 580 585 590  
320 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
321 595 600 605  
323 Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
324 610 615 620  
326 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp  
327 625 630 635 640  
329 Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
330 645 650 655  
332 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
333 660 665  
336 <210> SEQ ID NO: 3  
337 <211> LENGTH: 50  
338 <212> TYPE: DNA

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/807,721

DATE: 05/21/2002

TIME: 15:54:11

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\05212002\I807721.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

09302002 10:54:11  
DRAFT

7/3

## SEQUENCE LISTING

<110> AUBURN UNIVERSITY  
UNIVERSITY OF CENTRAL FLORIDA

<120> PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS

<130> 1463-PCT-00

<140> 09/807,721

<141> 2001-04-18

<150> PCT/US01/06274

<151> 2001-02-28

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 2059

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (17..1381, 1409..2050)

<400> 1

tctagaggag ggattt atg ggg gtc cag ctt cag cag tca gga cct gac 49  
Met Gly Val Gln Leu Gln Gln Ser Gly Pro Asp  
1 5 10

ctg gtg aaa cct ggg gcc tca gtg aag ata tcc tgc aag gct tct gga 97  
Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly  
15 20 25

tac aca ttc act gac tac aac ata cac tgg gtg aag cag agc cgt gga 145  
Tyr Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly  
30 35 40

aag agc ctt gag tgg att gga tat att tat cct tac aat ggt aat act 193  
Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Asn Gly Asn Thr  
45 50 55

tac tac aac cag aag ttc aag aac aag gcc aca ttg act gta gac aat 241  
Tyr Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn  
60 65 70 75

tcc tcc acc tca gcc tac atg gaa ctc cgc agc ctg aca tct gag gac 289  
Ser Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp  
80 85 90

tct gca gtc tat tac tgt gca acc tac ttt gac tac tgg ggc caa ggc 337  
Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly  
95 100 105

acc act ctc aca gtg agc tca gca tcc ccg acc agc ccc aag gtc ttc 385  
 Thr Thr Leu Thr Val Ser Ser Ala Ser Pro Thr Ser Pro Lys Val Phe  
 110 115 120  
  
 ccg ctg agc ctc gac agc acc ccc caa gat ggg aac gtc gtc gca 433  
 Pro Leu Ser Leu Asp Ser Thr Pro Gln Asp Gly Asn Val Val Val Ala  
 125 130 135  
  
 tgc ctg gtc cag ggc ttc ttc ccc cag gag cca ctc agt gtg acc tgg 481  
 Cys Leu Val Gln Gly Phe Phe Pro Gln Glu Pro Leu Ser Val Thr Trp  
 140 145 150 155  
  
 agc gaa agc gga cag aac gtg acc gcc aga aac ttc cca cct agc cag 529  
 Ser Glu Ser Gly Gln Asn Val Thr Ala Arg Asn Phe Pro Pro Ser Gln  
 160 165 170  
  
 gat gcc tcc ggg gac ctg tac acc acg agc agc cag ctg acc ctg ccg 577  
 Asp Ala Ser Gly Asp Leu Tyr Thr Ser Ser Gln Leu Thr Leu Pro  
 175 180 185  
  
 gcc aca cag tgc cca gac ggc aag tcc gtg aca tgc cac gtg aag cac 625  
 Ala Thr Gln Cys Pro Asp Gly Lys Ser Val Thr Cys His Val Lys His  
 190 195 200  
  
 tac acg aat tcc agc cag gat gtg act gtg ccc tgc cga gtt ccc cca 673  
 Tyr Thr Asn Ser Ser Gln Asp Val Thr Val Pro Cys Arg Val Pro Pro  
 205 210 215  
  
 cct ccc cca tgc tgc cac ccc cga ctg tcg ctg cac cga ccg gcc ctc 721  
 Pro Pro Pro Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu  
 220 225 230 235  
  
 gag gac ctg ctg tta ggt tca gaa gcg aac ctc acg tgc aca ctg acc 769  
 Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr  
 240 245 250  
  
 ggc ctg aga gat gcc tct ggt gcc acc ttc acc tgg acg ccc tca agt 817  
 Gly Leu Arg Asp Ala Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser  
 255 260 265  
  
 ggg aag agc gct gtt caa gga cca cct gag cgt gac ctc tgt ggc tgc 865  
 Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys  
 270 275 280  
  
 tac agc gtg tca tca gta ctt cct ggc tgt gcc cag cca tgg aac cat 913  
 Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His  
 285 290 295  
  
 ggg gag acc ttc acc tgc act gct gcc cac ccc gag ttg aag acc cca 961  
 Gly Glu Thr Phe Thr Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro  
 300 305 310 315  
  
 cta acc gcc aac atc aca aaa tcc gga aac aca ttc cgg ccc gag gtc 1009  
 Leu Thr Ala Asn Ile Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu Val  
 320 325 330  
  
 cac ctg ctg ccg ccg tcg gag gag ctg gcc ctg aac gag ctg gtg 1057

His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val  
 335 340 345  
 acg ctg acg tgc ctg gca cgt ggc ttc agc ccc aag gat gtc gtt 1105  
 Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val  
 350 355 360  
 cgc tgg ctg cag ggg tca cag gag ctg ccc cgc gag aag tac ctg act 1153  
 Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr  
 365 370 375  
 tgg gca tcc cgg cag gag ccc agc cag ggc acc acc acc tat gct gtc 1201  
 Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Tyr Ala Val  
 380 385 390 395  
 acc agc ata ctg cgc gtg gca gcc gag gac tgg aag aag ggg gag acc 1249  
 Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Glu Thr  
 400 405 410  
 ttc tcc tgc atg gtc ggc cac gag gcc ctg ccc ctg gcc ttc aca cag 1297  
 Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln  
 415 420 425  
 aag acc atc gac cgc ttg gcg ggt aaa ccc acc cat atc aat gtc tct 1345  
 Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser  
 430 435 440  
 gtt gtc atg gcg gag gcg gac ggc acc tgc tac aga tgaaatattg 1391  
 Val Val Met Ala Glu Ala Asp Gly Thr Cys Tyr Arg  
 445 450 455  
 cggatccgga gggattt atg gac att gtc atg acc cag tct cca gca atc 1441  
 Met Asp Ile Val Met Thr Gln Ser Pro Ala Ile  
 460 465  
 atg tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc 1489  
 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser  
 470 475 480  
 tca atg gta agt tac atg cac tgg ttc cag cag aag cca ggc act tct 1537  
 Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser  
 485 490 495  
 ccc aaa ctc tgg ctt tat agc aca tcc aac ctg gct tct gga gtc cct 1585  
 Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro  
 500 505 510  
 gct cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc 1633  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 515 520 525 530  
 agc cga atg gag gct gaa gat gct gcc act tat tac tgc cat caa agg 1681  
 Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg  
 535 540 545  
 act agc tac cca tac aca ttc gga ggg ggg acc aag ctt gag atc aaa 1729  
 Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys

550

555

560

cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 1777  
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
 565 570 575

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 1825  
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
 580 585 590

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 1873  
 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
 595 600 605 610

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 1921  
 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
 615 620 625

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 1969  
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
 630 635 640

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 2017  
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 645 650 655

ccc gtc aca aag agc ttc aac agg gga gag tgt tgatctaga 2059  
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 660 665

<210> 2  
 <211> 669  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly  
 1 5 10 15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp  
 20 25 30

Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu Glu Trp  
 35 40 45

Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn Gln Lys  
 50 55 60

Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr Ser Ala  
 65 70 75 80

Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr  
 85 90 95

Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val  
 100 105 110

Ser Ser Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Asp  
115 120 125

Ser Thr Pro Gln Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly  
130 135 140

Phe Phe Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln  
145 150 155 160

Asn Val Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp  
165 170 175

Leu Tyr Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro  
180 185 190

Asp Gly Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Ser Ser  
195 200 205

Gln Asp Val Thr Val Pro Cys Arg Val Pro Pro Pro Pro Cys Cys  
210 215 220

His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu  
225 230 235 240

Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala  
245 250 255

Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val  
260 265 270

Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser  
275 280 285

Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr Phe Thr  
290 295 300

Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala Asn Ile  
305 310 315 320

Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro  
325 330 335

Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu  
340 345 350

Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly  
355 360 365

Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln  
370 375 380

Glu Pro Ser Gln Gly Thr Thr Tyr Ala Val Thr Ser Ile Leu Arg  
385 390 395 400

Val Ala Ala Glu Asp Trp Lys Lys Gly Glu Thr Phe Ser Cys Met Val  
405 410 415

Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg  
420 425 430

Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser Val Val Met Ala Glu  
435 440 445

Ala Asp Gly Thr Cys Tyr Arg Met Asp Ile Val Met Thr Gln Ser Pro  
450 455 460

Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser  
465 470 475 480

Ala Ser Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly  
485 490 495

Thr Ser Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly  
500 505 510

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu  
515 520 525

Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His  
530 535 540

Gln Arg Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu  
545 550 555 560

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
565 570 575

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
580 585 590

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
595 600 605

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
610 615 620

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp  
625 630 635 640

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
645 650 655

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
660 665

<210> 3

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3  
aaaatctaga ggagggattt atgcagacat ctgtgtcccc ctcaaaagtc 50

<210> 4  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 4  
cataccgggg actagtcaca ttcacggtca cctcgcg 37

<210> 5  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 5  
Met Gln Thr Ser Val  
1 5

<210> 6  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 6  
Lys Asp Glu Leu  
1